In the Specification:

Please amend the specification as shown:

Please delete paragraphs [0056] to [0062] and replace them with the following paragraphs:

[0056] FIG. 9 provides maps of KB5008, pGL3-Control, KB5029, and KB5032. KB5008 carries a RSVLTR **(SEQ ID NO: 54)** promoter and was used to clone Ela and CREB. pGL3-Control carries a SV40 promoter and was used to clone Elb-19K and Bcl2. KB5029 carries the double expression cassettes for Ela and Elb-19K. KB5032 carries the double expression cassettes for CREB and Bcl2.

[0057] FIG. 10 provides the nucleotide coding sequence of Ela cDNA (SEQ ID NO: 40). **The amino acid sequence in Figure 10 is disclosed as SEQ ID NO: 48.**

[0058] FIG. 11 provides the nucleotide coding sequence of El A mutant Y47H (SEQ ID NO: 41). **The amino acid sequence in Figure 11 is disclosed as SEQ ID NO: 49.**

[0059] FIG. 12 provides the nucleotide coding sequence of hamster CREB-B cDNA. Amino acid residue Y134 is underscored (SEQ ID NO: 42). **The amino acid sequence in Figure 12 is disclosed as SEQ ID NO: 50.**

[0060] FIG. 13 provides the nucleotide coding sequence of hamster CREB-B mutant Y134F (SEQ ID NO : 43). **The amino acid sequence in Figure 13 is disclosed as SEQ ID NO: 51.**

[0061] FIG. 14 provides the nucleotide coding sequence of Elb-19K (SEQ ID NO: 44). **The amino acid sequence in Figure 14 is disclosed as SEQ ID NO: 52.**

[0062] FIG. 15 provides the nucleotide coding sequence of hamster Bcl2 deletion mutant Bcl2D (SEQ ID NO: 45). **The amino acid sequence in Figure 15 is disclosed as SEQ ID NO: 53.**

Please delete paragraph [0087] and replace it with the following paragraph:

[0087] In an alternative embodiment of this aspect of the invention, the variant Ela protein is a novel variant protein identified by screening or selecting a variant Ela defective in RB binding from a plurality of variant Ela proteins. A library of variant Ela proteins can be generated and screened in a microbial expression system for binding to RB. The library of variant Ela proteins is preferably a focused library in which sequence variation is restricted to particular regions of the Ela molecule. More preferably, mutations are restricted to the N-terminal (including CR1) and CR2 regions of Ela. For illustration, the library of variant Ela proteins may be expressed in *E. coli* as a fusion protein with a bacterial beta-lactamase and variants defective in RB binding selected using an *in vitro* selection system. For this purpose, RB protein or a fragment of RB capable of binding to wildtype Ela may be co-expressed with the Ela variant library. The RB fragment is co- expressed, for example, as a fusion protein with an inhibitor of beta-lactamase such as a BLIP protein and defective Ela variants are selected by their ability to prevent BLIP-fusion protein associating with beta-lactamase. In this way, *E. coli* cells containing a defective Ela are able to grow in the presence of the antibiotic ampicillin whereas cells containing Ela capable of binding RB are killed by this concentration of ampicillin. An example of a suitable BLIP protein is the BLIP from *Streptomyces clavuligerus* (Strynadka et al (1994) Nature 368: 657-660). The RB protein can be fused to either the carboxy-or amino- terminus of BLIP via a peptide linker such as a peptide of the sequence (Gly-Gly-Gly-Gly- Ser) **(SEQ ID NO: 55)** also designated (Gly4-Ser) **(SEQ ID NO: 55)** or multiples thereof. An example of a beta-lactamase protein is a masked beta-lactamase described in WO/03/069312. The Ela protein is fused to the

N- or C-terminus of beta-lactamase by a Gly4-Ser **(SEQ ID NO: 55)** linker peptide The masked beta- lactamase has reduced affinity for BLIP and binds BLIP detectably only in the presence of associated RB and Ela.

Please delete paragraph [0189] and replace it with the following paragraph:

[0189] Standard recombinant polymerase chain reaction methodology is employed to insert oligonucleotides encoding the HA epitope, (M)AYPDYVPDYAV **(SEQ ID NO: 56)**, at the 5' - end of the protein-coding sequence of *BCL-2* cDNA. The coding sequences are cloned into the vector pCI-neo (Promega) carrying a neomycin resistance gene or into a derivative vector carrying a hygromycin resistance gene. The authenticity of all constructs is verified by DNA sequencing.